Genetic dissection of assortative mating behavior

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Supporting Information: Figures S1

Figure S1. QTL analysis of variation of mate preference for individuals with alternative genotypes at LG18@0cM. QTL associated with the proportion of time males court H. melpomene (as opposed to H. cydno) females on chromosomes 17 for individuals homozygous (i.e. white, CYD:CYD = blue line) and heterozygous (i.e. red, CYD:MEL = orange line) at LG18@0cM. Dashed line represents log odds ratio (LOD) significance threshold (i.e. genome-wide alpha = 0.05) for heterozygous (i.e. red, CYD:MEL) individuals. Dashes along the x-axis indicate position of genetic markers (SNPs).